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                    GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

un on:        April 21, 2004, 04:08:30 ; Search time 1593.74 Seconds
                                (without alignments)
                              11386.553 Million cell updates/sec

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otal number of hits satisfying chosen parameters:    5815158

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description		
1	4025	100.0	4025	10	US-09-971-429B-15	Sequence 15, Appl
2	4025	100.0	4025	13	US-10-116-802-361	Sequence 361, App
3	4025	100.0	4025	14	US-10-002-600-46	Sequence 46, Appl
4	1997	49.6	3851	15	US-10-247-671-31	Sequence 31, Appl
5	1982	49.2	3775	9	US-09-954-456-2210	Sequence 2210, Ap
6	1982	49.2	3775	9	US-09-880-107-2221	Sequence 2221, Ap
7	1982	49.2	3775	10	US-09-960-706-649	Sequence 649, App
8	1982	49.2	3775	10	US-09-873-319-404	Sequence 404, App
9	1982	49.2	3775	10	US-09-873-367C-698	Sequence 698, App
10	1982	49.2	3775	15	US-10-205-823-133	Sequence 133, App
11	1982	49.2	3775	15	US-10-210-120-60	Sequence 60, Appl
12	1982	49.2	3775	15	US-10-004-113-17	Sequence 17, Appl
13	1982	49.2	3775	16	US-10-159-563-273	Sequence 273, App
14	1982	49.2	3775	17	US-10-394-948-11	Sequence 11, Appl
15	1965.4	48.8	3876	15	US-10-198-846-12898	Sequence 12898, A
16	1700	42.2	3632	16	US-10-144-194A-29	Sequence 29, Appl
17	1165	28.9	27184	15	US-10-004-113-16	Sequence 16, Appl
18	1165	28.9	27184	17	US-10-394-948-10	Sequence 10, Appl
19	797.4	19.8	1017	15	US-10-004-113-18	Sequence 18, Appl
20	797.4	19.8	1017	17	US-10-394-948-12	Sequence 12, Appl
21	796.2	19.8	4145	15	US-10-004-113-14	Sequence 14, Appl
22	796.2	19.8	4145	17	US-10-394-948-8	Sequence 8, Appli
23	657.2	16.3	1017	15	US-10-004-113-15	Sequence 15, Appli
24	657.2	16.3	1017	17	US-10-394-948-9	Sequence 9, Appli
25	401.4	10.0	561	15	US-10-029-386-3791	Sequence 3791, Ap
26	401.2	10.0	26993	15	US-10-004-113-13	Sequence 13, Appl
27	401.2	10.0	26993	17	US-10-394-948-7	Sequence 7, Appli
28	396.4	9.8	11176	9	US-09-738-968-43	Sequence 43, Appl
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32	279.2	6.9	2185	16	US-10-108-260A-1814	Sequence 2104, Ap
33	272	6.8	7634	15	US-10-311-455-2104	Sequence 23256, A
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38	226	5.6	7634	15	US-10-311-455-2103	Sequence 8755, Ap
39	224.2	5.6	655	15	US-10-198-846-13313	Sequence 440, App
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41	129.4	3.2	341	9	US-09-604-287A-440	Sequence 440, App
42	129.4	3.2	341	10	US-09-551-62-440	Sequence 440, App
43	129.4	3.2	341	10	US-10-007-805-440	Sequence 440, App
44	129.4	3.2	341	15	US-10-076-622-440	Sequence 440, App
45	129.4	3.2	341	15	US-10-124-805-440	

ALIGNMENTS

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(RESULT 1)
US-09-971-429B-15

; Sequence 15, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy K. W.
;  APPLICANT: Shyjan, Andrew W.
;  APPLICANT: Turner, Christopher M.
;  TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
;  FILE REFERENCE: PA-0040 US
;  CURRENT APPLICATION NUMBER: US/09/971,429B
;  CURRENT FILING DATE: 2001-10-04
;  PRIOR APPLICATION NUMBER: 60/239,024
;  PRIOR FILING DATE: 2000-04-10
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PERL Program
; SEQ ID NO 15
;  LENGTH: 4025
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No. US20030175704A1 1136056.1
US-09-971-429B-15

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Matches 4025;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db   3241 TGCCTGCATGAATAAACATTCACGTGCCCCTTTTCGCGCGTCTCCCATCCTGATTCCA 3300

Qy   3301 AGACCCATTCCTTAGCTAATTAATCCCCTTTCCGGAAGGCAATTATATC 3360
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Qy   3361 TATTATGTATAAGTAAATAATATTATATATGGATGTGTCGCCGTGCGCCGTGAGTG 3420
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Qy   3421 TGTGAGCGCTTCTGCAGCCGCTGCGCGCTGCGCGACCTAGGTTCACGTTGGGCCCTCAAAGCGGAGCCGTG 3480
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Qy   3481 AGAATTGGGAAACTGCTTCTTAGGAAACTCGGCTTCAACCCTGTCTCGGGCTGACCCCTTT 3540
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Qy   3541 TCTGATCGGTCTCCGCCCCCTGCTGATTGGTTCCCGATGGTCTCTCTCCTCCGTCTTTTGTC 3600
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Qy   3601 GCTCCGCGCTGTGTCCATCGACCCGTTTCACTTGTGCTCCTTCTGACTGTCCCCTGCCA 3660
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Db   3601 GCTCCGCGCTGTGTCCATCGACCCGTTTCACTTGTGCTCCTTCTGACTGTCCCCTGCCA 3660

Qy   3661 AATGCTCCAGCTGCGTCGCTGACTTCGTCGGGTTCGTTGGGGACATGAGATTTTATTTTTT 3720
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Qy   3721 GTTGAGTGAGACTGAGGGATGTGTAAGATTTTTACAACTCGTATCTCTTGACAACTTCTG 3780
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Qy   3841 TGAATCCCGACACCACCATCCACCAATGAATGTACTTGATGATTCTCTTATGTATGTAATTT 3900
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Qy   3901 TGCATCTGACCCCGGGGGTCTGGGGACAGATTGGCAATGGGACCGTCCCCTCAAACC 3960
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Qy   4021 AAAAA 4025
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                GenCore version 5.1.6

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M nucleic - nucleic search, using sw model

un on:     April 21, 2004, 04:08:30 ; Search time 1593.74 Seconds
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otal number of hits satisfying chosen parameters:      5815158

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ost-processing: Minimum Match 0%
             Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	% Score Match	Query Length	DB	ID	Description
1	4025	100.0	4025	10	US-09-971-429B-15	Sequence 15, Appl
2	4025	100.0	4025	13	US-10-116-802-361	Sequence 361, App
3	4025	100.0	4025	14	US-10-002-600-46	Sequence 46, Appl
4	1997	49.6	3851	15	US-10-247-671-31	Sequence 31, Appl
5	1982	49.2	3775	9	US-09-954-456-2210	Sequence 2210, Ap
6	1982	49.2	3775	9	US-09-880-107-2221	Sequence 2221, Ap
7	1982	49.2	3775	10	US-09-960-706-649	Sequence 649, App
8	1982	49.2	3775	10	US-09-873-319-404	Sequence 404, App
9	1982	49.2	3775	10	US-09-873-367C-698	Sequence 698, App
10	1982	49.2	3775	15	US-10-205-823-133	Sequence 133, App
11	1982	49.2	3775	15	US-10-210-120-60	Sequence 60, Appl
12	1982	49.2	3775	15	US-10-004-113-17	Sequence 17, Appl
13	1982	49.2	3775	16	US-10-159-563-273	Sequence 273, App
14	1982	49.2	3775	17	US-10-394-948-11	Sequence 11, Appl
15	1965.4	48.8		15	US-10-198-846-12898	Sequence 12898, A
16	1700	42.2		16	US-10-144-194A-29	Sequence 29, Appl
17	1165	28.9		15	US-10-004-113-16	Sequence 16, Appl
18	1165	28.9		17	US-10-004-948-10	Sequence 10, Appl
19	797.4	19.8		15	US-10-004-113-18	Sequence 18, Appl
20	797.4	19.8		17	US-10-394-948-12	Sequence 12, Appl
21	796.2	19.8		15	US-10-004-113-14	Sequence 14, Appl
22	796.2	19.8		17	US-10-394-948-8	Sequence 8, Appli
23	657.2	16.3		15	US-10-004-113-15	Sequence 15, Appl
24	657.2	16.3		17	US-10-394-948-9	Sequence 9, Appli
25	401.4	10.0		15	US-10-029-386-3791	Sequence 3791, Ap
26	401.2	10.0		15	US-10-004-113-13	Sequence 13, Appl
27	401.2	10.0		17	US-10-394-948-7	Sequence 7, Appli
28	396.4	9.8		9	US-09-738-968-43	Sequence 43, Appl
29	366.8	9.1		16	US-10-144-194A-27	Sequence 27, Appl
30	339.4	8.4		15	US-10-029-386-17491	Sequence 17491, A
31	334	8.3		15	US-10-198-846-9406	Sequence 9406, Ap
32	279.2	6.9		16	US-10-108-260A-1814	Sequence 1814, Ap
33	272	6.8	c	15	US-10-311-455-2104	Sequence 2104, Ap
34	243	6.0		13	US-10-027-632-23256	Sequence 23256, A
35	243	6.0		16	US-10-027-632-23256	Sequence 23256, A
36	230	5.7		13	US-10-027-632-106560	Sequence 106560,
37	230	5.7		15	US-10-027-632-106560	Sequence 106560,
38	226	5.6		15	US-10-311-455-2103	Sequence 2103, Ap
39	224.2	5.6		15	US-10-198-846-13313	Sequence 13313, A
40	148.6	3.7		10	US-09-918-995-8755	Sequence 8755, Ap
41	129.4	3.2	c	9	US-09-604-287A-440	Sequence 440, App
42	129.4	3.2	c	10	US-09-551-621-440	Sequence 440, App
43	129.4	3.2	c	14	US-10-007-805-440	Sequence 440, App
44	129.4	3.2	c	15	US-10-076-622-440	Sequence 440, App
45	129.4	3.2	c	15	US-10-124-805-440	Sequence 440, App

ALIGNMENTS

RESULT 1
US-09-971-429B-15

; Sequence 15, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 4025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 1136056.1
US-09-971-429B-15

Query Match   100.0%; Score 4025; DB 10; Length 4025;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 4025; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1 CATTCATAAGACTCAGAGCTCAGAGCTACGGCCACGGCAGGACACGCGGAACCAAGAACTTGGAAA 60

Qy   61 CTTGATTGTGTGGGTTCTTCTTCTTGGGGGTTATGAAATTCATTAATCTTTTTTTTCCGG 120
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Sequence 12898, A
Sequence 29, Appl
Sequence 16, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 8, Appli
Sequence 15, Appl
Sequence 9, Appli
Sequence 3791, Ap
Sequence 13, Appl
Sequence 7, Appli
Sequence 43, Appl
Sequence 27, Appl
Sequence 17491, A
Sequence 9406, Ap
Sequence 1814, Ap
Sequence 2104, Ap
Sequence 23256, A
Sequence 23256, A
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Sequence 13313, A
Sequence 8755, Ap
Sequence 440, App
Sequence 440, App
Sequence 440, App
Sequence 440, App
Sequence 440, App
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Page 2

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Qy  121  GGAGAAAGTTTTGGGAAAGATTCTTCCAGAATATTTCTTCATTTTCTTTTGGAGGACCG  180
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Db  121  GGAGAAAGTTTTGGGAAAGATTCTTCCAGAATATTTCTTCATTTTCTTTTGGAGGACCG  180

Qy  181  ACTTACTTTTTTTTGGTCTTCTTTATTATACTTTTTCCCCTTTTCCCCGGTGGGACCCC  240
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Qy  241  GCCGGACGGCCGTGGGAGGAGACCGTAGCTGAAGCTGATTTCGTGTGTTACAGCGTGTGCAC  300
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Db  241  GCCGGACGGCCGTGGGAGGAGACCGTAGCTGAAGCTGATTTCGTGTGTTACAGCGTGTGCAC  300

Qy  301  CAAGAGGCTTTCTGCCCCTGGGGGAGCAACCCTCCCTGGGTCCTACGGAGGC  360
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Qy  361  TGCACTTTCAAGAGGTACAGCGGCATCCGGCTCGTGGGGACCGGCACCGCAGCGGCACTGCA  420
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Qy  421  CAGAAAACTTGCCATTGTTGGAACGGACGTTGCGTCCTTCCCCGAGACTTCCCCGGACA  480
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Qy  481  GCGTACTTTGAGGACTCGCTCAGCGCGCACCGTGGGGACTCCCACGGCTCACCCCGGACTTG  540
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Qy  841  CTTGTGCAACCCAGCCTCATCTCTTCCATGGGCCCAGTGTGCAGCCACTGGCCT  900
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Qy  901  CCCAGCCCCGGTCGTCGAACCTAAGAAATGCGGGAAACCAGTTACTCCACACCAGGC  960
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Db  901  CCCAGCCCCGGTCGTCGAACCTAAGAAATGCGGGAAACCAGTTACTCCACACCAGGC  960

Qy  961  ATGAGTGCTACAGCAGTGGCCGGAGCCAGTGGTGTGGCAGTGGTGGCCTTCCACCAGCGGAACT  1020
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Qy  1021 ACCAGTGGCCTGGGCCTGCCCGCCCAGCCCGGCCTAGGAGACCCCGGAGGAG  1080
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Qy  1081 ACGTCACCCCAGAGGAAGCAGAAGACGAAGGGGTGCGCCCGGGACAACGAAATAAACTAGC  1140
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Qy  1141 AGCAGCTAAATGCAGGAGAACGGCGGCGGAACCGGCCGGAGGCGGAGCTGACCCGGACGAGCGAGACAG  1200
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Db  1261 GAGGAACGTCTGGAGTTGTGGCTGGTGGTCGCCCCACAAACCGGGCTGCAAGATCCCCTACG  1320
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Db  1621 AGCCTTTCCGATTCCCTGACTCGCCCTCCCTTCCGCTCTGCTCTGTGACTCTTTAGACAC  1680
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Qy  1741 AGGAGAGAGAGGGAAGAGACAAAGTGGGGTGTGCCATCGGACAGGAGGATTCCTTGTTGTTTTAGTCCTGC  1800

Db  1801 CTTCTCGCGGCCACTGCCGGCCACTGCCGGCACTGCGGAGGACGGAGACCTGGTGACTTGGGGGGGTGG  1860
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Qy  1801 CTTCTCGCGGCCACTGCCGGCCACTGCCGGCACTGCGGAGGACGGAGACCTGGTGACTTGGGGGGGTGG  1860

Db  1861 CTCTTGTAATCTGTCCCCGGAGGACGGAGGAGGTGGGGACAGGAGGAGGTGG  1920
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Db  1921 GAAGGGGATGGACACCCCAGCTGTTGGCTCTGACGTCAACCCAAGCTCTGGGG  1980
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Qy  1921 GAAGGGGATGGACACCCCAGCTGTTGGCTCTGACGTCAACCCAAGCTCTGGGG  1980

Db  1981 ATGGGGTGGGGAGGGGCGGGGGGGGCCCACCTTCGTGTGCAGTCCTGTGTGGGGATTAAGG  2040
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Qy  1981 ATGGGGTGGGGAGGGGCGGGGGGGGCCCACCTTCGTGTGCAGTCCTGTGTGGGGATTAAGG  2040

Db  2041 CGACCGGGTGCGTGCGAGGGTAGGCTGGAGGTGGCTGGAGGTCACTCTTCCCAGAGGAGGCT  2100
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Qy  2041 CGACCGGGTGCGTGCGAGGGTAGGCTGGAGGTGGCTGGAGGTCACTCTTCCCAGAGGAGGCT  2100

Db  2101 CAACAAGGGAAAAATGCCACTCCACACCCGATTTCG  2160
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Qy  2101 CAACAAGGGAAAAATGCCACTCCACACCCGATTTCG  2160

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Db  2221 TCCATGGTGTGAGATCCTCTTTACTTCTAGGGCAGAAGTGAGCCCCCTTAAAGGGAA  2280
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Db  2281 TTCGATGCCCCCTAGAATAATCTCATCCCCCACCGGACGTTCGTGTTTGAGATGTGAA  2340
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Qy  2281
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Thu Apr 2

Apr 22 11:49:09 2004

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Qy   3421 TGTGAGGGCTTCGCAGCCTTCGCAGCCTGCGGACCTAGGTTCACGTTGGCGGCCCTCAAAGCGAGCCGTG 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TGTGAGGGCTTCGCAGCCTTCGCAGCCTGCGGACCTAGGTTCACGTTGGGCGCCCTCAAAGCGAGCCGTG 3480

Qy   3481 AGAATTGGGAAACTCTGGCTTCTAGGAAACTCTGGCTTCTAGGAAACTCTGGCTTCAACCCTGTCTCGGGGCTGACCCTTT 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 AGAATTGGGAAACTCTGGCTTCTAGGAAACTCTGGCTTCAACCCTGTCTCGGGGCTGACCCTTT 3540

Qy   3541 TCTGATGCTCTCGGCCCCTGCTGATTGTTCCCGATGGTCTCTCCCTCTGTCTCTTTGTC 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCTGATGCTCTCGGCCCCTGCTGATTGTTCCCGATGGTCTCTCCCTCTGTCTCTTTGTC 3600

Qy   3601 GCTCCGCCTGTGTCCATCTGACCCGTTTCACTTGTCGCTCCTTTCTGACTGTCCCTGCCA 3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GCTCCGCCTGTGTCCATCTGACCCGTTTCACTTGTCGCTCCTTTCACTTGTCCCTGCCA 3660

Qy   3661 AATGCTCCAGCTGCGTCGCTTCTGACTTCTCGGGGTTCGTTGGGACATGAGATTTATTTTTT 3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 AATGCTCCAGCTGCGTCGCTTCTGACTTCTCGGGGTTCGTTGGGACATGAGATTTATTTTTT 3720

Qy   3721 GTTGAGTGAGACTGAGGGATCGTAAGATGTCGTGTATCTCTTGACACTTCTG 3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GTTGAGTGAGACTGAGGGATCGTAAGATTTTACAACTCTGTATCTCTTGACAACTTCTG 3780

Qy   3781 GGTGCGAGATGTGATGAGATGTGAGACAGGGCTTGACTCATGACTCATGACAACAAATCAAA 3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGTGCGAGATGTGATGAGATGTGAGACAGGGCTTGACTCATGACTCAACAACAAATCAAA 3840

Qy   3841 TGAATCCGACACACCATCCACCAATGAATGTACTTGATGATTCTCTTATGTAATTT 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAATCCGACACACCATCCACCAATGAATGTACTTGATGATTCTCTTATGTAATTT 3900

Qy   3901 TGCATCTGACCCCCGGGGGTCTGGGACAGATTGGCAATGGGACCGTCCCCTCTAAACC 3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TGCATCTGACCCCCGGGGGTCTGGGACAGATTGGCAATGGGACCGTCCCCTCTAAACC 3960

Qy   3961 TTGCCCCTCGCCCTCGTTGCCAATTAAAAGCTCTTAAAAACGCAAAAAAGCAAAGGATTTA 4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 TTGCCCCTCGCCCTCGTTGCCAATTAAAAGCTCTTAAAAACGCAAAAAAGCAAAGGATTTA 4020

Qy   4021 AAAAA 4025
          |||||
Db   4021 AAAAA 4025
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RESULT 2

Query Match   100.0%; Score 4025; DB 13; Length 4025;
Best Local Similarity   100.0%; Pred. No.0;
Matches 4025; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   2281 TTCGATGCCCCCTAGAATAATCTCATCCCCACCGCGACGTTCGTGTTGAGATGTGAA 2340

Qy   2341 CGTCCTTCCTTGACCTGTCTAGCCACTCCACTCCCCAGAAATAAGCTGGCTCGTATTCGG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CGTCCTTCCTTGACCTGTCTAGCCACTCCACTCCCCAGAAATAAGCTGGCTCGTATTGG 2400

Qy   2401 TATTTCTGGCCTCGCTAAGGGCTCCCCACCCCTGATTAAGTCATGCCCTCATGCGCCTTG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TATTTCTGCCTCGCTAAGGGCTCCCCACCCCTGATTAAGTCATGCCCTCATGCGCCTTG 2460

Qy   2461 CTTTCTGACTGACATGTGTTTTCCTCAGTGGATCCTGCCACCGCGGCGTGCCAGCCGAGCCC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTTTCTGACTGACATGTGTTTTCCTCAGTGGATCCTGCCACCGCGGCGTGCCAGCCGAGCCC 2520

Qy   2521 GCTGCGTGGCCTTCCTCGTTCTGATTTCATGCGCAGTCAGGGTGCTGCTGT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GCTGCGTGGCCTTCCTCGTTCTGATTTCATGCGCAGTCAGGGTGCTGCTGT 2580

Qy   2581 GAATGCCGTCCTGCTGGGAGTGAGTGATTTATAACCTGTGAAATGAGTTGGCCAGATTGTGGGG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GAATGCCGTCCTGCTGGGAGTGAGTGATTTATAACCTGTGAAATGAGTTGGCCAGATTGTGGGG 2640

Qy   2641 GTGCAGCTGGGCTGGGGGCAGCACCTCATGGGGGGGATAAATGTCCGGGCACTTCCTCG 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GTGCAGCTGGGCTGGGGGCAGCACCTCATGGGGGGGATAAATGTCCGGGCACTTCCTCG 2700

Qy   2701 AAAGCCGTTTCCTGCGGTCTCCCGTTCGCGTGCATCCCCGTTCTTCCTCCCCTCCCTCAACAG 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 AAAGCCGTTTCCTGCGGTCTCCCGTTCGCGTGCATCCCCGTTCTTCCTCCCCTCCCTCAACAG 2760

Qy   2761 CAGAGTTAGACTCAATGGGCTGACAGAACCGACGAATGGGGGTGACACGTCCTCGCAAT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CAGAGTTAGACTCAATGGGCTGACAGAACCGACGAATGGGGGTGACACGTCCTCGCAAT 2820

Qy   2821 GCCACTGTCGGCCTCGGCCTCGTCGTCTCGTCCTCAGGAGCCTCCAGCCTGTGTC 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCACTGTCGGCCTCGGCCTCGTCGTCTCGTCCTCAGGAGCCTCCAGCCTGTGTC 2880

Qy   2881 TTCGTTTAATGGTCCCCGACCTAATCCCAGACACTAGGACGCCAACTTCTCACCACCCC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TTCGTTTAATGGTCCCCGACCTAATCCCAGCACTAGGACGCCAACTTCTCACCACACCCC 2940

Qy   2941 TTGGCCCCTCACATCCTCTACCTGGAAGGGAGTGAGGGGCTGTGACTAATTTTTCTCGGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TTGGCCCCTCACATCCTCTACCTGGAAGGGAGTGAGGGGCTGTGACTAATTTTTCTCGGA 3000

Qy   3001 CAAGAGTCATATGCTTCGAGTGCTTCGGTTCGGTACCCCACAAAACCCACAATATTTTGGACTGG 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CAAGAGTCATATGCTTCGAGTGCTTCGGTACCCCACAAAACCCACAATATTTTGGACTGG 3060

Qy   3061 CAGACTTCAAGGGGCTGGAATCTCATGGAATTCATGCCGATTCCGCCATCCCTGACCA 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAGACTTCAAGGGGCTGGAATCTCATGGAATTCATGCCGATTCCGCCATCCCTGACCA 3120

Qy   3121 TGGTTTTTGGCTCTCCACCCCGCCGTTCCCTGACGCTTCATCTTCATGGAGGGATTTCTT 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TGGTTTTTGGCTCTCCACCCCGCCGTTCCCTGACGCTTCATCTTCATGGAGGGATTTCTT 3180

Qy   3181 TATGGAGGCAAATTTATATTTTTATATATCGGGGGTGGACCACGACCCCTCCATCCG 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TATGGAGGCAAATTTATATTTTTATATATCGGGGGTGGACCACGACCCCTCCATCCG 3240

Qy   3241 TGCCTGCATGAATAAACATTCCACGTGCCCCTTTTTCGGCGCTGGTTCCCATCCTGATTCCA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGCCTGCATGAATAAACATTCCACGTGCCCCTTTTTCGGCGCTGGTTCCCATCCTGATTCCA 3300

Qy   3301 AGACCCATTTCCTTAGCTAATTAATCCCTTTTCCTTTTCCTGGGTTTCCGGAAAGGCAATTATATC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGACCCATTTCCTTAGCTAATTAATCCCTTTTCCTGGGTTTCCGGAAAGGCAATTATATC 3360

Qy   3361 TATTATGTATAAGTAAATATATTATATATATGGATGTGTGTGTGCCGTGCGCCGTGAGTG 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TATTATGTATAAGTAAATATATTATATATATGGATGTGTGTGTGCCGTGCGCCGTGAGTG 3420
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